

```

1 MVRSGNKA VVLCMDVGF TMSNIPGIESPFEQAKKVITMFVQRQVFAEN 50
  |||||
1 MVRSGNKA VVLCMDVGF TMSNIPGIESPFEQAKKVITMFVQRQVFAEN 50

51 KDEIALVLF GTDGTDNPLSGGDQYQNITVHRHMLPDPFDLLEDIESKIOP 100
  |||||
51 KDEIALVLF GTDGTDNPLSGGDQYQNITVHRHMLPDPFDLLEDIESKIOP 100

101 GSQQADF LDAIVSMDVIQHETIGKKFEKRRHIEIFTDLSSRFSKSQLDII 150
  |||||
101 GSQQADF LDAIVSMDVIQHETIGKKFEKRRHIEIFTDLSSRFSKSQLDII 150

151 IHSLKKCD ISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGPFPLKGITEQ 200
  |||||
151 IHSLKKCD ISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGPFPLKGITEQ 200

201 QKEGLEIV KMVMISLEGEDGLDEIYSFSESLRKLCVFKKIERHSIHWPCR 250
  |||||
201 QKEGLEIV KMVMISLEGEDGLDEIYSFSESLRKLCVFKKIERHSIHWPCR 250

```

Fig. 1

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDKTLKKEDIQETVYCLNDD 300  
 |||||  
 251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDKTLKKEDIQETVYCLNDD 300  
 . . .  
 301 DETEVLKEDIQGFYRGSDIVPFSKVDEEQMKYKSEGKCFVSLGFCKSSQ 350  
 |||||  
 301 DETEVLKEDIQGFYRGSDIVPFSKVDEEQMKYKSEGKCFVSLGFCKSSQ 350  
 . . .  
 351 VQRRFFMGNQVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400  
 |||||  
 351 VQRRFFMGNQVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400  
 . . .  
 401 ANPQVGVAFFPHIKHNYECLVYVQLPFMEDLRQYMFSSLNKSKKYAPTEAQ 450  
 |||||  
 401 ANPQVGVAFFPHIKHNYECLVYVQLPFMEDLRQYMFSSLNKSKKYAPTEAQ 450  
 . . .  
 451 LNAVDALIDMSLAKKDEKTDLTLEDLFPPTTKIPNPRFQRLFQ 492  
 |||||  
 451 LNAVDALIDMSLAKKDEKTDLTLEDLFPPTTKIPNPRFQRLFQ 492

Fig. 1 (Cont..)

[illegible]

Fig. 2.

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300  
 |||||  
 251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300  
 . . . . . 304  
 301 DETE..... 304  
 ||||  
 301 DETEVLKEDIQFRYGSDIVPFSKVDEEQMKYSEKCFVLGFKSSQ 350  
 . . . . . LNPPAEVTTKSQIPLSKIKTLFPLIEAKKQDQVTA 339  
 |||||  
 501 PREPLPIQQHINMLNPPAEVTTKSQIPLSKIKTLFPLIEAKKQDQVTA 550  
 . . . . . 389  
 340 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 389  
 |||||  
 551 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 600  
 . . . . . 439  
 390 LVKQKKASFEESASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFS 439  
 |||||  
 601 LVKQKKASFEESASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFS 650

Fig. 2 (Cont.)

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440 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAEE 489
      |||||
651 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAEE 700
      |||||
      490 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 521
            |||||
      701 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 732

```

**Fig. 2 (Cont.)**

2 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51  
 |||||  
 1 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50  
 .  
 52 EGSNPPASPLQDNLVIALHSYEP SHDGLGFEKGEQLRILEQSGEWWKAQ 101  
 |||||  
 51 EGSNPPASPLQDNLVIALHSYEP SHDGLGFEKGEQLRILEQSGEWWKAQ 100  
 .  
 102 SLTTGQEGFIPNFVAKANSLEPEPWF FKNLSRKDAERQLLAPGNTHGSF 151  
 |||||  
 101 SLTTGQEGFIPNFVAKANSLEPEPWF FKNLSRKDAERQLLAPGNTHGSF 150  
 .  
 152 LIRESESTAGSFSLSVRDFDQNGEVV KHKYKIRNLDNGGFYISPRITFPG 201  
 |||||  
 151 LIRESESTAGSFSLSVRDFDQNGEVV KHKYKIRNLDNGGFYISPRITFPG 200  
 .  
 202 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETLKLVERL 251  
 |||||  
 201 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETLKLVERL 250

Fig. 3

252 GAGQFGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MKQLQHQLV 301  
 |||||  
 251 GAGQFGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MKQLQHQLV 300  
 |||||  
 302 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLD MAAQIAEG 351  
 |||||  
 301 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLD MAAQIAEG 350  
 |||||  
 352 MAFIEERNYIHRDLRAANILVSDTL SCKIADFGLARLIEDIHHQVR 397  
 ||||| : |  
 351 MAFIEERNYIHRDLRAANILVSDTL SCKIADFGLARLIEDNEYTAR 396

Fig. 3 (Cont.)

302 TLKLVRLGAGQFGEVVMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 351  
 |||||  
 243 TLKLVRLGAGQFGEVVMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 292  
 .  
 352 QLQHRLVRLYAVVTQEPIYIITEYMENGSLVD FLKTPSGIKLTINKLLD 401  
 |||||  
 293 QLQHRLVRLYAVVTQEPIYIITEYMENGSLVD FLKTPSGIKLTINKLLD 342  
 .  
 402 MAAQIAEGMAFIEERNYIHRDLRAANILVSDT LSCKIADFG LARLIEDNE 451  
 |||||  
 343 MAAQIAEGMAFIEERNYIHRDLRAANILVSDT LSCKIADFG LARLIEDNE 392  
 .  
 452 YTAREGAKFPIKWTAPEAINYGFTTIKSDVWSFG ILLTEIVTHGRIPYPG 501  
 |||||  
 393 YTAREGAKFPIKWTAPEAINYGFTTIKSDVWSFG ILLTEIVTHGRIPYPG 442  
 .  
 502 MTNPEVIQNLERGYRMVRPDCNCP EELYQLMRLCWKERPEDRPTFDYLR SV 551  
 |||||  
 443 MTNPEVIQNLERGYRMVRPDCNCP EELYQLMRLCWKERPEDRPTFDYLR SV 492  
 .  
 552 LEDFFTATEGQYQPQP 567  
 |||||  
 493 LEDFFTATEGQYQPQP 508

Fig. 4 (Cont.)



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2 GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51
  |||||
1 GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50
52 EGSNPPASPLQGDPRQGLKDKACGSLAVGFHLSPTYFLPGLAFLVPHPV 101
  |||||
51 EGSNPPASPLQ..... 61
102 TPGFLPIPARFSLTPLVFTDNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 151
  |||||
62 .....DNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 92
152 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 201
  |||||
93 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 142
202 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGQEVVKHYKIRNLDNGGFYI 251
  |||||
143 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGQEVVKHYKIRNLDNGGFYI 192
252 SPRIITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRE 301
  |||||
193 SPRIITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRE 242

```

Fig. 4

1 MRIAVICFLLGITCAIPVKQADSGSSEKQLYNKYPDAVATWLNPDPSQ 50  
 |||||  
 1 MRIAVICFLLGITCAIPVKQADSGSSEKQLYNKYPDAVATWLNPDPSQ 50  
 51 KQNLAPQNAVSSSEETNDFKQETLPSKSNEHDMDDMDEDDDDHVDQS 100  
 |||||  
 51 KQNLAPQNAVSSSEETNDFKQETLPSKSNEHDMDDMDEDDDDHVDQS 100  
 101 DSIDSNSDDVDDTDDSHQSDSHHSDSEDELVTDFPTDLPATEVFTPVV 150  
 |||||  
 101 DSIDSNSDDVDDTDDSHQSDSHHSDSEDELVTDFPTDLPATEVFTPVV 150  
 151 PTVDTYDGRGDSVVYGLRSKSKKFRRPDIQVNPLTD 186  
 |||||  
 151 PTVDTYDGRGDSVVYGLRSKSKKFRRPDIQYPDATD 186

Fig. 5

```

62  AEAIPCTLAVSNPHTDAWKSHGLVEVASYCEESRGNQWVPYISLQER 109
    | : | | . | | | | | | | | | | | | | | | | | | | |
114 ARDLHC.LLVTNPHTDAWKSHGLVEVASYCEESRGNQWVPYISLQER 160

```

**Fig. 6**

1 MRARPQVCEALLFALALQTVGCYGIKWIALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 1 MRARPQVCEALLFALALQTVGCYGIKWIALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCCSSIELAPNY 100  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCCSSIELAPNY 100  
 |||||  
 101 LLDLERTRESAFVYALSAAISHAIARACTSGDLPGCSCGPVGP 150  
 |||||  
 101 LLDLERTRESAFVYALSAAISHAIARACTSGDLPGCSCGPVGP 150  
 |||||  
 151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200  
 |||||  
 151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200  
 |||||  
 201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250  
 |||||  
 201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250

Fig. 7

```

251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
    |||||
251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
    |||||
301 KTSNGSDSCDLM.....CCYVTCRRCERTVER 327
    |||||
301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350
    |||||

328 YVCK 331
    |||
351 YVCK 354

```

Fig. 7(Cont.)

ॐ  
ॐ  
ॐ

184 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 233  
 |||||  
 301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350

234 YVCK 237  
 ||||  
 351 YVCK 354

Fig. 8 (Cont.)

1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50  
 |||  
 1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50  
 |||  
 51 TMYPPWDSTFDHINKGRVMQIIIVKGKNVDLISSETVELYSLAERCCKNN 100  
 |||  
 51 TMYPPWDSTFDHINKGRVMQIIIVKGKNVDLISSETVELYSLAERCCKNN 100  
 |||  
 101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRRAIK 150  
 |||  
 101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRRAIK 150  
 |||  
 151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200  
 |||  
 151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200  
 |||  
 201 CIDKVIKCTGSAINSRFTMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250  
 |||  
 201 CIDKVIKCTGSAINSRFTMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250  
 |||  
 251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300  
 |||  
 251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300  
 |||

Fig. 9



301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350  
 |||||  
 301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350  
 . . .  
 351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFGKVFLAEFK 400  
 |||||  
 351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFGKVFLAEFK 400  
 . . .  
 401 KTNQFFAIAKALKKDVVLMDDDVECTMVEKRVLSLAWEHFELTHMFCTFQT 450  
 |||||  
 401 KTNQFFAIAKALKKDVVLMDDDVECTMVEKRVLSLAWEHFELTHMFCTFQT 450  
 . . .  
 451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500  
 |||||  
 451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500  
 . . .  
 501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550  
 |||||  
 501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

Fig. 9 (Cont.)

```

551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
    |||||
551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
    |||||

601 WLEKEAKDLLVKV 613
    |||||
601 WLEKEAKDLLVKI 613

```

Fig. 9(Cont.)

1 MPITRMRPWLEMQINSQIPGLIWINKKEEMIFQIPWKHAAKHGWDINK 50  
 |||| ||||| ||||| ||||| ||||| : ||||| ||||| |||||  
 1 MPITWMRPWLEMQINSQIPGLIWINKKEEMILEIPWKHAAKHGWDINK 50  
 .  
 51 DACLFRSWAIHTGRYKAGEKEPDPTWKANFRCAMNSLPDIEEVKDQSRN 100  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 DACLFRSWAIHTGRYKAGEKEPDPTWKANFRCAMNSLPDIEEVKDQSRN 100  
 .  
 101 KGSSAVRVYRMLPPLTKNQKERSKSSRDAKSKAKRKSCGDSSPDTFSD 150  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 KGSSAVRVYRMLPPLTKNQKERSKSSRDAKSKAKRKSCGDSSPDTFSD 150  
 .  
 151 GLSSSTLPDDHSSYTVPGYMQDLEVEQALTPALSPCAVSSTLPDWHIPVE 200  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 151 GLSSSTLPDDHSSYTVPGYMQDLEVEQALTPALSPCAVSSTLPDWHIPVE 200  
 .  
 201 VVPDSTSDLYNFQVSPMPSTSEATTDEDEEGKLPEDIMKLLSEQSEWQPTN 250  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 201 VVPDSTSDLYNFQVSPMPSTSEATTDEDEEGKLPEDIMKLLSEQSEWQPTN 250  
 .  
 251 VDGKGYLLNEPGVQPTSVYGFDFSCKEEPEIDSPGG 285  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 251 VDGKGYLLNEPGVQPTSVYGFDFSCKEEPEIDSPGG 285

Fig. 10

1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPGAPVEVESFLVHPGDL 50  
 |||||  
 1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPGAPVEVESFLVHPGDL 50

51 LQLRCRLRDDVQSIINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100  
 |||||  
 51 LQLRCRLRDDVQSIINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100

101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150  
 |||||  
 101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150

151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200  
 |||||  
 151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200

201 HRIGGYKVRATWSIIMDSVVPDCKGNYTCIVENEYGSINHTYQLDVVER 250  
 |||||  
 201 HRIGGYKVRATWSIIMDSVVPDCKGNYTCIVENEYGSINHTYQLDVVER 250

251 SPHRPILQAGLPANKTVALGSNVFEMCKVYSDPPQPHIQWLKHIEVNGSKI 300  
 |||||  
 251 SPHRPILQAGLPANKTVALGSNVFEMCKVYSDPPQPHIQWLKHIEVNGSKI 300

**Fig. 11**

301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCIAGNSIGLS 350  
 |||||  
 301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCIAGNSIGLS 350  
 |||||  
 351 HHSAWLTVLEALEERPAMVTSPLYLEIIYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 351 HHSAWLTVLEALEERPAMVTSPLYLEIIYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 401 SGTKKSDFHSMQAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLS 450  
 |||||  
 401 SGTKKSDFHSMQAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLS 450  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFQVVLAEAI GL 500  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFQVVLAEAI GL 500  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNI INLLGA 550  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNI INLLGA 550  
 |||||

Fig. 11 (Cont.)

551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDL 600  
 |||||  
 551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDL 600  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHH 650  
 |||||  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHH 650  
 651 IDYYKKTNGRLPVKWMapealeFDRIYTHQSDVWSFGV 688  
 |||||  
 651 IDYYKKTNGRLPVKWMapealeFDRIYTHQSDVWSFGV 688

Fig. 11(Cont.)

2 PKRGKKGVAEDGDELRTPEAKKSKTAAKKNDKEAAGEGPALYEDPPDQ 51  
 |||||  
 1 PKRGKKGVAEDGDELRTPEAKKSKTAAKKNDKEAAGEGPALYEDPPDQ 50  
 .  
 52 KTSPSGKPATLKICSWNVVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSE 101  
 |||||  
 51 KTSPSGKPATLKICSWNVVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSE 100  
 .  
 102 NKLPaelQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGI..... 146  
 |||||  
 101 NKLPaelQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEH 150  
 .  
 147 .....AYVPNAGRGLVRLEYRQRWD EAERKFLKGLAS 178  
 |||||  
 151 DQEGRVIVAEFDSEFVLVTAYVPNAGRGLVRLEYRQRWD EAERKFLKGLAS 200  
 .  
 179 RKPLVLCGDLNVAHEEIDLNPKNKKNAGFTPQERQGFGE LLQAVPLAD 228  
 |||||  
 201 RKPLVLCGDLNVAHEEIDLNPKNKKNAGFTPQERQGFGE LLQAVPLAD 250

Fig. 12

229 SFRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYELLSHSLPALCDSKIR 300  
 251 SFRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYELLSHSLPALCDSKIR 278

**Fig. 12(Cont.)**



2 PKRGKKGAVAEDGDELRTGKGMKSALLPRNCGGVCHSLDVREPEAKSK 51  
 |||||  
 1 PKRGKKGAVAEDGDELRT.....EPEAKSK 26  
 52 TAAKNDKEAAGEGPALYEDPPDQKTPSGKPA TLKICSWNVDGLRAWIK 101  
 |||||  
 27 TAAKNDKEAAGEGPALYEDPPDQKTPSGKPA TLKICSWNVDGLRAWIK 76  
 102 KKGLDWVKEEAPDILCLQETKCSENKLP AELQELPGLSHQYWSAPSDKEG 151  
 |||||  
 77 KKGLDWVKEEAPDILCLQETKCSENKLP AELQELPGLSHQYWSAPSDKEG 126  
 152 YSGVGLLSRQCPLKVSYGIGDEEHDQEG RVIVAEEDSFVLVTAYVPNAGR 201  
 |||||  
 127 YSGVGLLSRQCPLKVSYGIGDEEHDQEG RVIVAEEDSFVLVTAYVPNAGR 176  
 202 GLVRL EYRQRWDEAFRKFLKGLASRKPLVLC GDLNVAHEEIDL RNPKNK 251  
 |||||  
 177 GLVRL EYRQRWDEAFRKFLKGLASRKPLVLC GDLNVAHEEIDL RNPKNK 226

Fig. 13

252 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 301  
 |||||  
 227 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 276  
 302 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPIITLYLAL 342  
 |||||  
 277 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPIITLYLAL 317

Fig. 13(Cont.)

1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50  
 |||||  
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50  
 |||||  
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 100  
 |||||  
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 100  
 |||||  
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 150  
 |||||  
 101 LAFLNFQNNLQQTPPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHL 150  
 |||||  
 101 LAFLNFQNNLQQTPPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHL 200  
 |||||  
 151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 200  
 |||||  
 151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 250  
 |||||  
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250  
 |||||  
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 14

251 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 300  
|||||  
251 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 300

301 DEV 303

||.

301 DEL 303

Fig. 14 (Cont.)

1 MFQAAERPQEWAMEGPRDGLKRLDDRHDSGLDSMKDEEYEQMVKEIQ 50  
 |||||  
 1 MFQAAERPQEWAMEGPRDGLKRLDDRHDSGLDSMKDEEYEQMVKEIQ 100  
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 100  
 |||||  
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 150  
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 150  
 |||||  
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 183  
 151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNG..... 200  
 |||||  
 151 ACEQGCLASVGVLTSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 222  
 184 .....QEPNCGR TALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250  
 |||||  
 201 LLVSLGADVNAQEPNCGR TALHLAVDLQNPDLVSLLLKCGADVNRVTYQG

Fig. 15

```

223 YSPYQLTWGRPSTRIOQLGQLTLENLQMLPESEDEESYDTESEFFTEFFE 272
|||||
251 YSPYQLTWGRPSTRIOQLGQLTLENLQMLPESEDEESYDTESEFFTEFFE 300
|||||

273 DELPYDDCVFEGGQRLTL 289
|||||
301 DELPYDDCVFEGGQRLTL 317

```

Fig. 15 (Cont.)

```

1 MAGIFYAFSCIFGICDAVTGSRVYPANEVTLILDSRSVQELGWIASPL 50
|||||
1 MAGIFYAFSCIFGICDAVTGSRVYPANEVTLILDSRSVQELGWIASPL 50
|||||
51 EGGWEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRLTDWITREGAQRVYIE 100
|||||
51 EGGWEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRLTDWITREGAQRVYIE 100
|||||
101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENQFKIDTIAA 150
|||||
101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENQFKIDTIAA 150
|||||
151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFOQDVGCIALVSVRVE 200
|||||
151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFOQDVGCIALVSVRVE 200
|||||
201 YKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250
|||||
201 YKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250
|||||
251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDATCAKCPPHSYV 300
|||||
251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDATCAKCPPHSYV 300

```

Fig. 16

Fig. 16 (Cont.)



601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFFGEVCSGRLKVPKGKREICV 650  
 |||  
 601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFFGEVCSGRLKVPKGKREICV 650  
 .  
 651 AIKTLKAGYTDKQRRDFLSEASIMGQFDHPNIIHLEGVVTKCKPVMIIITE 700  
 |||  
 651 AIKTLKAGYTDKQRRDFLSEASIMGQFDHPNIIHLEGVVTKCKPVMIIITE 700  
 .  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 |||  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 .  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAPEAIAIRK 800  
 |||  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAPEAIAIRK 800  
 .  
 801 FTSASDVWSYGIWMWEVMSYGERPYWDMNSQD..... 832  
 |||  
 801 FTSASDVWSYGIWMWEVMSYGERPYWDMNSQDVIIKAIIEEGYRLPPPMDCP 850  
 .  
 833 .....PNT 835  
 |||  
 851 IALHQLMLDCWQKERSDRPKFGQIVNMMLDKLIRNPNSLKRITGTESSRPNT 900

Fig. 16 (Cont.)



1 MNDEGIKNMDQVAPVANSYRGTLKRQPAFDTFDGLFAVFPSLNEEQTLQ 50  
 |||||  
 1 MNDEGIKNMDQVAPVANSYRGTLKRQPAFDTFDGLFAVFPSLNEEQTLQ 50  
 51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKATFSGF..... 90  
 |||||  
 51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKATFSGFKKEQRRRLGIP 100  
 91 .....FWATNEEFLVNVLQRFGMNGQMLCNLCKERFLEL 125  
 |||||  
 101 KNPWLWSEQQVCQWLLWATNEEFLVNVLQRFGMNGQMLCNLCKERFLEL 150  
 126 APDFVGDILWEHLEQMIKENQEKTEQYEENSHLTSVPHWINSNTLGFGT 175  
 |||||  
 151 APDFVGDILWEHLEQMIKENQEKTEQYEENSHLTSVPHWINSNTLGFGT 200  
 176 EQAPYGMQTQNYPKGGLLDSMCPASTPSVLSSSEQEFQMFPKSRLSSVSVT 225  
 |||||  
 201 EQAPYGMQTQNYPKGGLLDSMCPASTPSVLSSSEQEFQMFPKSRLSSVSVT 250  
 226 YCSVSQDFPGSNLNLTTNNSGTPKDHDPENGADSFESSDLLQSWNSQS 275  
 |||||  
 251 YCSVSQDFPGSNLNLTTNNSGTPKDHDPENGADSFESSDLLQSWNSQS 300

Fig. 17

325  
326 SLLDVQRPVSFEFEDDCSQSLCNKPTMSFKDYIQERSDPVEQGKPVIP 325  
301 SLLDVQRPVSFEFEDDCSQSLCNKPTMSFKDYIQERSDPVEQGKPVIP 350  
326 AAVLAGFTGSGPIQLWQFLELLSDKSCQSFISWTGDGWEFKLADPDEVA 400  
351 AAVLAGFTGSGPIQLWQFLELLSDKSCQSFISWTGDGWEFKLADPDEVA 425  
376 RRWGKRKNKPKMNYEKL SRGLRYYDKNIIHKTSGRYVYRFVCDLQNL 450  
401 RRWGKRKNKPKMNYEKL SRGLRYYDKNIIHKTSGRYVYRFVCDLQNL 444  
426 GFTPEELHAILGVQPDTE 444  
451 GFTPEELHAILGVQPDTE 469

Fig. 17 (Cont.)

1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50  
 |||||  
 1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50  
 51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGICECQYQFRHRRWNC 100  
 |||||  
 51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGICECQYQFRHRRWNC 100  
 101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSACREGELSTCGCS 150  
 |||||  
 101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSACREGELSTCGCS 150  
 151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200  
 |||||  
 151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200  
 201 ILMNLHNNAGRRTVVYNLADVACKCHGVSGCSLKTCLWLQADFRKVGDA 250  
 |||||  
 201 ILMNLHNNAGRRTVVYNLADVACKCHGVSGCSLKTCLWLQADFRKVGDA 250  
 251 LKEKYDT 257  
 |||||  
 251 LKEKYDS 257

Fig. 18

1 MALRRSMGRPGLPPLPLPPPPRLGILLAEESAAAGLKLIMGAPVKLTVSQGG 50  
 |||||  
 1 MALRRSMGRPGLPPLPLPPPPRLGILLAEESAAAGLKLIMGAPVKLTVSQGG 50  
 51 PVKLNCSEGMEEPDIQWVKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100  
 |||||  
 51 PVKLNCSEGMEEPDIQWVKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100  
 101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150  
 |||||  
 101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150  
 151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTGTQSTMFSCAEHNL 200  
 |||||  
 151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTGTQSTMFSCAEHNL 200  
 201 KGLASSRTATVHLQALPAAPFNITVTKLSSSNASVAVWMPGADGRALLQSC 250  
 |||||  
 201 KGLASSRTATVHLQALPAAPFNITVTKLSSSNASVAVWMPGADGRALLQSC 250  
 251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSRLRVCANALGPSP 300  
 |||||  
 251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSRLRVCANALGPSP 300

Fig. 19

301 YADWVPFQTKGLAPASAPQNLHAIRTDGSLLEWEEVPEAPLEGPLGPY 350  
 |||||  
 301 YADWVPFQTKGLAPASAPQNLHAIRTDGSLLEWEEVPEAPLEGPLGPY 350  
 |||||  
 301 YADWVPFQTKGLAPASAPQNLHAIRTDGSLLEWEEVPEAPLEGPLGPY 400  
 |||||  
 351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVCGPWSQP 400  
 |||||  
 351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVCGPWSQP 450  
 |||||  
 401 LVVSSHDRAGQQGPPHSRTSWPVVLGVLTALVTAAALALLRKRKKE 450  
 |||||  
 401 LVVSSHDRAGQQGPPHSRTSWPVVLGVLTALVTAAALALLRKRKKE 500  
 |||||  
 451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGSDELKE 500  
 |||||  
 451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGSDELKE 550  
 |||||  
 501 EDVLIPEQQFTLGRMLGKGEFGSVREAQLKQEDGSFVKVAVKMLKADII 550  
 |||||  
 501 EDVLIPEQQFTLGRMLGKGEFGSVREAQLKQEDGSFVKVAVKMLKADII 600  
 |||||  
 551 SSDIEEFLREAAACMKKEFDHPHVAKLVGVSLRSRAKGRLPIMVILPFMKH 600  
 |||||  
 551 SSDIEEFLREAAACMKKEFDHPHVAKLVGVSLRSRAKGRLPIMVILPFMKH 600

Fig. 19 (Cont.)

601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSSRNFIHRDLAA 650  
 |||||  
 601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSSRNFIHRDLAA 650  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSDCRY 678  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSGDYY 678

Fig. 19(Cont.)



**Fig. 20**

301 NGMLRYRIVSQAPSTPSPNMFNTINNETGDIITVAAGLDREKVQQYTLIIQ 350  
 |||||  
 301 NGMLRYRIVSQAPSTPSPNMFNTINNETGDIITVAAGLDREKVQQYTLIIQ 350  
 . . . . .  
 351 ATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPENRVDIIV 400  
 |||||  
 351 ATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPENRVDIIV 400  
 . . . . .  
 401 ANLTVTDKQDQPHTPAWNNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVVKPI 450  
 |||||  
 401 ANLTVTDKQDQPHTPAWNNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVVKPI 450  
 . . . . .  
 451 DFETNRMFVLTVAAEENQVPLAKGIQHPPQSTATVSVTIDVNENPYFAPN 500  
 : |||||  
 451 DFETNRMFVLTVAAEENQVPLAKGIQHPPQSTATVSVTIDVNENPYFAPN 500  
 . . . . .  
 501 PKIIRQEEGLHAGTMLTTFQAQDPDRYMQQNIRYTKLSDPANWLKIDPVN 550  
 |||||  
 501 PKIIRQEEGLHAGTMLTTFQAQDPDRYMQQNIRYTKLSDPANWLKIDPVN 550  
 . . . . .  
 551 GQITTIADVLDRESPNVKNNIYNATFLASDNGIPPMMSGTGTQIYLLDIND 600  
 |||||  
 551 GQITTIADVLDRESPNVKNNIYNATFLASDNGIPPMMSGTGTQIYLLDIND 600

Fig. 20 (Cont.)

```

601 NAPQVLPQEAETCETPDNPNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650
|||||
601 NAPQVLPQEAETCETPDNPNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650

651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700
|||||
651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700

701 CQCDNSGDCCTDVRIVGAGLGTGAIIAILLIILVLMFVVMKRRD 750
|||||
701 CQCDNSGDCCTDVRIVGAGLGTGAIIAILLIILVLMFVVMKRRD 750

751 KERQAKQLLIDPEDDVRDNILKYDEEGGGEEDQDYDLSQLQQPDTVPEPDA 800
|||||
751 KERQAKQLLIDPEDDVRDNILKYDEEGGGEEDQDYDLSQLQQPDTVPEPDA 800

801 IKPVGIRRMDERPIHAEPQYPVRSAAAPHPGDIGDFINE 838
|||||
801 IKPVGIRRMDERPIHAEPQYPVRSAAAPHPGDIGDFINE 838

```

Fig. 20 (Cont.)



```

11 NVQILLEAASYLEQIEKENKKCEHGYASSFPSPRLQHSKPPRRLSRA 60
   ||| |||| :||. ||: ||||| ||||| ||||| ||||| |||||
8 NVQRLLEAAEFLERRERE...CEHGYASSFPSPRLQHSKPPRRLSRA 54
   . . . . .
61 QKHSSGSSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGDCRHT 110
   |||||.||||| ||||| ||||| ||||| ||||| ||||| |||||
55 QKHSSGTSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGDCRHT 104
   . . . . .
111 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 160
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
105 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 154
   . . . . .
161 RIRMSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTTSISDIDD 210
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
155 RIRMSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTTSISDIDD 204
   . . . . .
211 HSSLPSIGSDEGYSSASVKLSFTS 234
   ||||| ||||| ||||| ||||| |||||
205 HSSLPSIGSDEGYSSASVKLSFTS 228

```

Fig. 22

```

1 MESPASSQPASMPQSKGSKRKKDLRISCMSKPPAPNPPTPRNLDSTRFI 50
  |||
1 MESPASSQPASMPQSKGSKRKKDLRISCMSKPPAPNPPTPRNLDSTRFI 50

51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVN 100
  |||
51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVN 100

101 SQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
  |||
101 SQEQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150

151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200
  |||
151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200

201 EGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
  |||
201 EGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250

```

Fig. 23

```

251 VWSLGITMIEMAILRFPYESWGTPFQQLKQVVEEPSQLPADRFSPFFVD 300
|||||
251 VWSLGITMIEMAILRFPYESWGTPFQQLKQVVEEPSQLPADRFSPFFVD 300
|||||
301 FTAQCLRKKNPAERMSYLELI 320
|||||
301 FTAQCLRKKNPAERMSYLELM 320

```

Fig. 23(Cont.)

```

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTSVVVLQLE 50
  |||||
1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTSVVVLQLE 50

51 KEEQIHSVDIGNDGS AFVEVLVGSSAGGAGEQDYEVLLVTSSEFMSPSESR 100
  |||||
51 KEEQIHSVDIGNDGS AFVEVLVGSSAGGAGEQDYEVLLVTSSEFMSPSESR 100

101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150

151 SPDDKDEAEAPSQKVTVTKLGFQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
151 SPDDKDEAEAPSQKVTVTKLGFQFRVKEEDESANSLRPGALFFSRINKTSP 200

201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242

```

Fig. 24



```

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||
1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50

51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESR 100
  |||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESR 100

101 SGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150
  |||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150

151 SPDPKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||
151 SPDPKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200

201 VTASDPAGPSYAAATLQASSAASSASPVSRIGSTSKPQESS.....DF 244
  |||
201 VTASDPAGPSYAAATLQASSAASSASPVSRIGSTSKPQESPCKGRKLDL 250

245 GVEEERSWRPQSIPIPSAP 264
  |.. :| . || |
251 NQEEKKTPSKPPAQLSPSPV 270

```

Fig. 25

[illegible]

**Fig. 26**

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50  
 |||  
 1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50  
 |||  
 51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSFMSPSES 100  
 |||  
 51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSFMSPSES 100  
 |||  
 101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150  
 |||  
 101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150  
 |||  
 151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200  
 |||  
 151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200  
 |||  
 201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESPKGKRKLDL 250  
 |||  
 201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESPKGKRKLDL 250  
 |||  
 251 NOEEKKTPSKPPAQLSPSPVKRPKLPAPTRTPATAVPARAQAVTGKPR 300  
 |||  
 251 NOEEKKTPSKPPAQLSPSPVKRPKLPAPTRTPATAVPARAQAVTGKPR 300  
 |||

Fig. 27

```

301 GEGTEPRRPRAGPEELGKILQGVVVVLSGFQNPFRSELRDKALELGAKYR 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 GEGTEPRRPRAGPEELGKILQGVVVVLSGFQNPFRSELRDKALELGAKYR 350
    .
351 PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRKEWVLDCHRMRRRLPSRR 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRKEWVLDCHRMRRRLPSRR 400
    .
401 YLMAGPGSSSEEDASHSGSGDEAPKLPQKQPQTKTKPTQAAAGPSSPQK 450
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 YLMAGPGSSSEEDASHSGSGDEAPKLPQKQPQTKTKPTQAAAGPSSPQK 450
    .
451 PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRAEAEQKE 500
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRAEAEQKE 500
    .
501 HRLPPGQEEENGEDPYAGSTDENTDSEEHQEPDLPVPPELPRFLPGQ 546
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 HRLPPGQEEENGEDPYAGSTDENTDSEEHQEPDLPVPPELPRFLPGQ 546

```

Fig. 27(Cont.)

1 MAGAIASRMSFSSLKRKQPKTFTVRIVTMDAEMEFCNCKWKGDLDLV 50  
 |||||  
 1 MAGAIASRMSFSSLKRKQPKTFTVRIVTMDAEMEFCNCKWKGDLDLV 50  
 . . . . .  
 51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDSKEEPTFFHFLAKF 100  
 |||||  
 51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDSKEEPTFFHFLAKF 100  
 . . . . .  
 101 YPENAEELVQEITQHLFFLQVKKQILDKEIYCPPEASVLLASYAVQAKY 150  
 |||||  
 101 YPENAEELVQEITQHLFFLQVKKQILDKEIYCPPEASVLLASYAVQAKY 150  
 . . . . .  
 151 GDYDPSVHKRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRAR 200  
 |||||  
 151 GDYDPSVHKRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRAR 200  
 . . . . .  
 201 DEAEEMEYLKIAQDLEMYGVNYFAIRNKKGTCELLGVDALGLHIYDPENRL 250  
 |||||  
 201 DEAEEMEYLKIAQDLEMYGVNYFAIRNKKGTCELLGVDALGLHIYDPENRL 250  
 . . . . .  
 251 TPKISFPWKNEIRNISYSKDEFTIKPLDKKIDVFKFNSSKLRVNKLILQL 300  
 |||||  
 251 TPKISFPW.NEIRNISYSKDEFTIKPLDKKIDVFKFNSSKLRVNKLILQL 299

Fig. 28

301 CIGNHDLFMRRRKADSLFVQOMKAQAREEKARK..... 333  
 |||||  
 300 CIGNHDLFMRRRKADSLFVQOMKAQAREEKARKQMERQRLAREKQMRREEA 349  
 334 .....OMKEEATMANEALMRSEETADLLAEKAQITTEEEAKLLA 371  
 |||||  
 350 ERTRDELERLLQMKEEATMANEALMRSEETADLLAEKAQITTEEEAKLLA 399  
 372 QKAAEAEQEMQRIKATAIRTEEEKRLMEQKVLEAEVLALKMAEESERRAK 421  
 |||||  
 400 QKAAEAEQEMQRIKATAIRTEEEKRLMEQKVLEAEVLALKMAEESERRAK 449  
 422 EADQLKQDLQEAAREAEERRAKQKLLLEIATKPTYPPMNPAPLPDIPSFN 471  
 |||||  
 450 EADQLKQDLQEAAREAEERRAKQKLLLEIATKPTYPPMNPAPLPDIPSFN 499  
 472 LIGDSLFSDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 521  
 |||||  
 500 LIGDSLFSDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 549  
 522 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFEEEL 567  
 |||||  
 550 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFEEEL 595

Fig. 28 (Cont.)



1 MDLEGRNGGAKKKNFFKLNKSEKDKKPKTVSVFSMFRYSNWLDKLY 50  
 |||  
 1 MDLEGRNGGAKKKNFFKLNKSEKDKKPKTVSVFSMFRYSNWLDKLY 50  
 51 MVVGTIAAIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100  
 |||  
 51 MVVGTIAAIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100  
 101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAIYQVSFWCLAAGRQIHKIRKQ 150  
 |||  
 101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAIYQVSFWCLAAGRQIHKIRKQ 150  
 151 FFHAIMRQEIIGWFDVHDVGEINTRLTDDVSKINEVIGDKIGMFFQSMATF 200  
 |||  
 151 FFHAIMRQEIIGWFDVHDVGEINTRLTDDVSKINEVIGDKIGMFFQSMATF 200  
 201 FTGFIVGFTRGWKLTLVILAISPVGLSAAVWAKILSSFTDKELLAYAKA 250  
 |||  
 201 FTGFIVGFTRGWKLTLVILAISPVGLSAAVWAKILSSFTDKELLAYAKA 250  
 251 GAVAEVLAARTVIAFGGQKKELELYNKNLEEAKRIGIKKAITANISIG 300  
 |||  
 251 GAVAEVLAARTVIAFGGQKKELELYNKNLEEAKRIGIKKAITANISIG 300

Fig. 30



301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASP 350  
 |||||  
 301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASP 350  
 . . .  
 351 SIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFS 400  
 |||||  
 351 SIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFS 400  
 . . .  
 401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTEGM 450  
 |||||  
 401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTEGM 450  
 . . .  
 451 VSDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVTMDEI 500  
 |||||  
 451 VSDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVTMDEI 500  
 . . .  
 501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550  
 |||||  
 501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550  
 . . .  
 551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIA 600  
 |||||  
 551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIA 600

Fig. 30 (Cont.)

601 FDDGVIVEKGNHDELMKEKGIYFKLVMTMQTAGNEVELENAADESKSEIDA 650  
 |||||  
 601 FDDGVIVEKGNHDELMKEKGIYFKLVMTMQTAGNEVELENAADESKSEIDA 650

651 LEMSSNDSRSSLIRKRSTRRSVRGSAQDRKLSTKEALDESIPVSWFRI 700  
 |||||  
 651 LEMSSNDSRSSLIRKRSTRRSVRGSAQDRKLSTKEALDESIPVSWFRI 700

701 MKLNLTEWPFVVGVFCAIINGGLQPAFAIFSKIIGVTRIDDPETKRQ 750  
 |||||  
 701 MKLNLTEWPFVVGVFCAIINGGLQPAFAIFSKIIGVTRIDDPETKRQ 750

751 NSNLFSLFLALGIISFTTFELQFTFGKAGEILTKRLRYMVFRSMLRQD 800  
 |||||  
 751 NSNLFSLFLALGIISFTTFELQFTFGKAGEILTKRLRYMVFRSMLRQD 800

801 VSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNIANLGTGIIIS 850  
 |||||  
 801 VSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNIANLGTGIIIS 850

851 FIYGWQLTLLLLAIVPIIAAGVVMKMLSGQALKDKKELEGAGKIATEA 900  
 |||||  
 851 FIYGWQLTLLLLAIVPIIAAGVVMKMLSGQALKDKKELEGAGKIATEA 900

Fig. 30 (Cont.)

901 IENFRTVSLTQEQKFEHMYAQLQVPRNSLRKAHIFGITFSFTQAMMY 950  
 |||||  
 901 IENFRTVSLTQEQKFEHMYAQLQVPRNSLRKAHIFGITFSFTQAMMY 950  
 . . . . .  
 951 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGVSSFAFDYAK 1000  
 |||||  
 951 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGVSSFAFDYAK 1000  
 . . . . .  
 1001 AKISAAHIIMIIEKTPLIDSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 |||||  
 1001 AKISAAHIIMIIEKTPLIDSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 . . . . .  
 1051 PVLQGLSLEVKKGTALVSSGCGKSTVVQLLERFYDPLAGKVLLDGKE 1100  
 |||||  
 1051 PVLQGLSLEVKKGTALVSSGCGKSTVVQLLERFYDPLAGKVLLDGKE 1100  
 . . . . .  
 1101 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDN SRVVSQEEIVRAAK 1150  
 |||||  
 1101 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDN SRVVSQEEIVRAAK 1150  
 . . . . .  
 1151 EANIHA FIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHILLDD 1200  
 |||||  
 1151 EANIHA FIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHILLDD 1200

1201 EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGR 1250  
 |||||  
 1201 EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGR 1250  
 .  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277  
 |||||  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277

Fig. 30(Cont.)

```

1 MDLEGNRGGAKKKNEFFKLNKSEKDKKEKPTVSVFSMFRYSNWLDKLY 50
  |||||
1 MDLEGNRGGAKKKNEFFKLNKSEKDKKEKPTVSVFSMFRYSNWLDKLY 50

51 MVVGTLAAILHGAGLPLMLLVFGEMTDIFANAGNLEDLMSNITNRSNDIND 100
  |||||
51 MVVGTLAAILHGAGLPLMLLVFGEMTDIFANAGNLEDLMSNITNRSNDIND 100

101 TGFFMNLEEDMTRYAAYYSYGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150
  |||||
101 TGFFMNLEEDMTRYAAYYSYGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150

151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMATF 200
  |||||
151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200

201 FTGFI VGTFRGWKLTFLVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250
  |||||
201 FTGFI VGTFRGWKLTFLVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250

251 GAVAEVLA AIRT V IAFGGQKKELERYNKNL EEA KRIGIKKAITANISIG 300
  |||||
251 GAVAEVLA AIRT V IAFGGQKKELERYNKNL EEA KRIGIKKAITANISIG 300

```

Fig. 31

301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFFSVLIGAFSVGQASP 350  
 |||||  
 301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFFSVLIGAFSVGQASP 350  
 . . .  
 351 SIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFS 400  
 |||||  
 351 SIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFS 400  
 . . .  
 401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMORLYDPTEGM 450  
 |||||  
 401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMORLYDPTEGM 450  
 . . .  
 451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500  
 |||||  
 451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500  
 . . .  
 501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550  
 |||||  
 501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550  
 . . .  
 551 ILLLDEATSALDTESEAEVQAALDKVSR 578  
 ||||| :  
 551 ILLLDEATSALDTESEAVVQVALDKARK 578

Fig. 31(Cont.)

1 MSRSKRDNNFYSEIGDSTFTVLKRYQNLKPIGSAQGI VCAAYDAILER 50  
 |||||  
 1 MSRSKRDNNFYSEIGDSTFTVLKRYQNLKPIGSAQGI VCAAYDAILER 50  
 . . .  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIGLLNVFT POKSLEE 100  
 |||||  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIGLLNVFT POKSLEE 100  
 . . .  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLH SAGIIHR 150  
 |||||  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLH SAGIIHR 150  
 . . .  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRY YRAPEVILGM 200  
 |||||  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRY YRAPEVILGM 200

201 GYKENTE 207

||||| :

201 GYKENVD 207

Fig. 32

1 MSRSKRDNNFYSEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50  
 |||||  
 1 MSRSKRDNNFYSEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPQKSLEE 100  
 |||||  
 51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPQKSLEE 100

101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150  
 |||||  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150

151 DLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200  
 |||||  
 151 DLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200

201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250  
 |||||  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250

251 KLQPTVRTYVENRPRKYAGYSFEKLFDPDVLFPADSEHNKILKASQ 293  
 |||||  
 251 KLQPTVRTYVENRPRKYAGYSFEKLFDPDVLFPADSEHNKILKASQ 293

Fig. 33



1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50  
 |||||  
 1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50  
 . . . . .  
 51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPPQKSLEE 100  
 |||||  
 51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPPQKSLEE 100  
 . . . . .  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150  
 |||||  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150  
 . . . . .  
 151 DLKPSNIVVKS DCTLKILD FGLARTAGTSEMMTPYVVTRYRAPEVILGM 200  
 |||||  
 151 DLKPSNIVVKS DCTLKILD FGLARTAGTSEMMTPYVVTRYRAPEVILGM 200  
 . . . . .  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250  
 |||||  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250

Fig. 34

[illegible]

**Fig. 34(Cont.)**

7 arsgfyrqevtktaewravryrdlqpvgsgaygavcsavdgrtgakvaik 56  
 |||||  
 1 ARSGFYRQEVTKTAEVRAVRYRDLQPVGSGAYGAVCSAVDGRGTGAKVAIK 50  
 57 klyrpfqselfakrayrelrlklmrhenviglldvftpdetlddftdfy 106  
 |||||  
 51 KLYRPFQSELF AKRAYRELRLKLMRHENVIGLLDVFTPDETLDDFTDFY 100  
 107 lvmpfmngtdlgklmkheklgedriqlvyqmlkglyryihaagihrdlkp 156  
 |||||  
 101 LVMPFMGTDLGKLMKHEKLGEDRIQLVYQMLKGLRYIHAAGIIHR.VSP 149  
 157 gnlavne 163  
 | | .:  
 150 GGEAAHQ 156

Fig. 35

```

1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKP 50
  |||||
1 MSPFLRIGLSNFDGSCQSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKP 50

51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETTVELYSLAERCCKNN 100
  |||||
51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETTVELYSLAERCCKNN 100

101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150

151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200

201 CIDKVIKCTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCCT 250
  |||||
201 CIDKVIKCTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCCT 250

```

Fig. 36

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMIESTQQ 300  
 |||||  
 251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMIESTQQ 300

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350  
 |||||  
 301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350

351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKGSFGKVFLAEFK 400  
 |||||  
 351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKGSFGKVFLAEFK 400

401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHPPFLTHMFCTFQT 450  
 |||||  
 401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHPPFLTHMFCTFQT 450

451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500  
 |||||  
 451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500

Fig. 36 (Cont.)

501 VYRDLKLDNILLDKDGHKIADFGMCKENMLGDAKNTFCGTPDYIAPEI 550  
 |||||  
 501 VYRDLKLDNILLDKDGHKIADFGMCKENMLGDAKNTFCGTPDYIAPEI 550  
 551 LLGQKYNHSVDWWSFGVLLYEMLLIGQSPFHGQDEEEELFHSIRMDNPFYPR 600  
 |||||  
 551 LLGQKYNHSVDWWSFGVLLYEMLLIGQSPFHGQDEEEELFHSIRMDNPFYPR 600  
 601 WLEKEAKDLLVK..VRSEAKSVFIR 623  
 |||||  
 601 WLEKEAKDLLVKLFVREPEKRLGVR 625

Fig. 36 (Cont.)